

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(I) APPLICANT: THE NATIONAL UNIVERSITY OF SINGAPORE

(ii) TITLE OF INVENTION: DIAGNOSIS OF PARASITES

10

(iii) NUMBER OF SEQUENCES: 22

(iv) CORRESPONDENCE ADDRESS:

15

(A) ADDRESSEE: DAVIES COLLISON CAVE

(B) STREET: 1, LITTLE COLLINS STREET

(C) CITY: MELBOURNE

(D) STATE: VIC

(E) COUNTRY: AUSTRALIA

(F) ZIP: 3000

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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

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(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT INTERNATIONAL

(B) FILING DATE: 6-FEB-1998

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: AU P04953

(B) FILING DATE: 6-FEB-1997

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: AU P06329

(B) FILING DATE: 21-APR-1997

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(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: AU P09481

(B) FILING DATE: 26-SEP-1997

(A) NAME: HUGHES, E. J. L.

(A) TELEPHONE: 61 3 9254 2777

(B) TELEFAX: 61 3 9254 2770

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5849 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

15 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20	TAATGAAGCT GTACATCCTT CTAAATATCC AACATATGCA AATTCACCTG CTATTAATAA	60
	AGTACGTTCA AATTGTGCAA AATCATAAGA ATTAGTCTTA AAATAAGTTG ATAAATTAAA	120
25	ACTACATTTT ATATACTTAG ACACATAACA AAAAGATCCT TCACTAAAAA TAATTGAATT	180
	AATATTTGCA AAAAAATTAT CTTTATAAGA AACTACAGTT CCTAAATATT TTTTACTAA	240
	TAAAGGATAT TTTAAATAA CGTCCAATAA AGACAAAAAT ATAATACCTA ATTTTTTTAA	300
30	AAAATATTGT GTTGATATGA AAACAGATAT ACTATCACAA ATAACATCAA TAGGAATTAT	360
	TTTTTTATTA AAATAGGTAT CTAAAAAATT TATATTTAAA TTAGTTTTTA AATATACTAA	420
35	CAAATTACTA TCITTTTAAAG TAGAAGAATA ATAAATAATA TTATCATAAC TAATATTGGG	480
	ACATTCGAAA CACGACCAAT CTGGTAATTT AAACATATTT AAAAATTTTA AAGAATATAT	540
	TTTAAATTTG TAAATAAAAA AATATAAATA AATATTATTA GATAAATTTT TTATCAAATT	600

	TTTATTTAAT CCATTTCTTA TTAAATATAA ATTTATTTTA TTATTATATT GATATTTATA	660
	ATTTAAATTA TAAATATTTA AAAATTTTTT TAATTTTAAT TTATTTATCA TAATAATTTT	720
5	ATATTATAAA ATATTTCAAG TTAACGATGA GATTTGAAC TACAATCTAC TGATTACAAA	780
	TCAGTTGCTT TACCAATTAA GCCACTTTAA CAAATATAAT ATTTATAATT AAATATTCAA	840
	CTTATTAGGA ATTATACACA AAATATATTA CTATAAATAC ATATTAATTC TATAAAATAA	900
10	TTTTTCTAAT TATTGTTTTA TTCATTTATA TGATTAGAAT ATTATTTTTA ATTAAATTTT	960
	CTTATTTATA TTACTTCAAC AATTAAAATT TTATACTTAA CTACTCAACA TTACAAAATA	1020
15	TAATAATTGA TATATCATTG GTATAATTTT TTCGATCCTC TCGTACTAGA AAAAATAATT	1080
	TCAATATTCT AACACTTATA TTAGATATGG ACCGAAC TGT CACGACGT TCTGAACCCA	1140
	GCTCACGTAT CGCTTTAATA GGCGAACAGA CTTACCCTTA AAACATACTA CTGCCTTAGG	1200
20	ATGCGATAAG CCGACATCGA GGTGCCAAAC CTTTTCGTCA ATATGGACTC TCGGAAAAGA	1260
	TTAGCCTGTT ATCCCTAGAG TAACTTTTAT CCGTTAAGCG ATAATTTTAT TATTAAATAA	1320
25	TTATCGGATC ATTAAGACCG ACATTAATCT CTGTTTAATT TGTAAATTTT ACAGTTAATT	1380
	ATATATTTAT CTTTATATAA TAAATATAAC ATTGTACACC TCCGTTTTTA TATAGGAGGA	1440
	GACCGCCCCA GTCAAATAT CTTATAAATA TTGTTAAAAA TTTTGTATA AAAATTTTAT	1500
30	AAGAATTTAT ATATATATAA AATGGTATTT CATTACAAT TACATTATTT CCAAAAAAAT	1560
	AATATTACTA CTTCCCATTT ATTCTATGTT ATATATATAT ATTTTCAATA TCTATTAATA	1620
35	GTAAGCTTC ATAGGGTCTT TCTGTCCTAA TATAAGAAAT CTGCATCTTC ACAGATAATT	1680
	TTATTTCAAT AAGATTTTTT TTAAGACAGC ATTTAAGTCG TTACATCTTT CATGCAGGTC	1740
	GGAACCTTACC CGACAAGGAA TTTGCTACC TTTGGACCGT TATAGATACA GCCGCCGTTT	1800
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	ACTATAGCTT ATATATATAT TATAATTTTA AATTATAAAT ATTATTTTTC CATAATAGCA	1860
	CTGGGCAGAT GTCAATCTTT ATACATCATC TTTCGATTTC GCAAAGATTT GTGTTTTTGT	1920
5	TAAACAGTCG CTTAAATTTT TTGTTTTCAA CTAAATAAGT ATCTCTTCTC CCCTAAGTTT	1980
	ACGAGATAAA TTTGCCGAGT TCCTTAAAAA AAATTATCTC AACTTCTTAA TAATTTATAT	2040
10	ATATTTACTA GTGTCAGTTT ACAGTACGAA TACATAATAA TATATATATA TAAATAATTT	2100
	TTATATAATA TAATATATTT ATTATTATAT TAGTTTTAAA ATATAAATAT TATTATATAG	2160
	TATAAGAATA TTAACCTTATT ACCTATCGAT TACACATTAC ATCTCATCTC AAGATACGAC	2220
15	TAACCCCTATT TAAAATAATA ATAAATAGGA GCCCTTAAAT TATAGAAGTA TTGGATTTTT	2280
	ACCAATATTT ACATTACTCA AATTAGCATT ATCACTTTTG ATATAATTAT TTAACTTTTT	2340
20	CATATAAATA ATTTATATTC AAAACGCTCT TTTACCAATT TAATTTTATT AATATTAAAT	2400
	TTTATACATA TCGATAATTA ATTTATTTTC GATTATTTCT GAACTAAAAT TACTAAATTA	2460
	ATGAGCTTTT ACGCACTCTT TAAAAGATAA CTGCTTCTAA ATTTACTTTT TAATTATTTA	2520
25	AATAATTTTA TATTCTTTTT AAGACTTAAT TAATATTTAA AAATCTTAAT TTATAATTCG	2580
	GGCTGTTTTCC CTTTTGAAAA TAAAGCTTAT CCTTTATTTT CTGATCATAT ATATATTTTA	2640
30	TTAAATAAAA TTCTTAAATT ATTTTCATTA ATATTAACCTA TATAAATTAA TTTAATAAAA	2700
	AAAGAGTTTT ACATTTATTT ATATATAAAT ACTATACTTA CATATATTTT AAAGAGAACC	2760
	AGCTATCTTC AAATTCGATT GGCATTTTAC CTCTAATTAT ACTTTATTTG ATACTTTTGC	2820
35	AACAGTAACC AATTCAACT TCAATTTAAT TTTATTTAAA TCTTATTTTA AATATAATTA	2880
	GATCATTTGA TTTCGGTCT ATAATAAATA ATATACTAAA TGCTTATTAT ATATAATAAC	2940
40	AAACTCGAGT ATACTTTGGC TTCATTTATA AATATTTAAC CTAATAATTA TACTATTTAT	3000

TATAACTTGC TAATTCTTTC TTCAACAAGA AAATAATAAA ATTATATTAA ATTTTATTAT 3060

TATTTATTAA ATTTAAAATT CAGGTTCTTT TCACTATTTT CTCAAAATCC TTTTCATCTT 3120

5 TCCCTCACGG TACTATTCAC TATCAACTTT TATTATATTA AATTTTATAA GATAACTCTT 3180

AATTATATTT ATATTATTCA TATAAAATAT ATTTTATAT TACTTAATTA AAATTTTACA 3240

TATATAATGT TTTAAATCTT TCAGTTCGCT CGCCACTACT ATGAAAATCG TTATTACTTT 3300

10 ATATTCCCTT AAGTACTAAG ATGATTCAGT TCCTTAAGTT TTTTAAAT ATTTATATAA 3360

AAATAAATTT TTATTCAGAT ACTTTTATAA TTTTAATAAT AAAAAATTTT AAATATATTT 3420

15 AATTTTTTAT AATTATAAAA ATTCGTAA TATATTTAAC GTCTTCTTC AATAATAAAA 3480

ATAATAGACA TCCTTTTAAA TTTATTATAT ATATTTAATT ATATATTTAA CTATATAAAT 3540

TATAAATTAA TTTATTTAAA ATAAGCGAAA AACGSAATTG AACCGATTAC CTTCGGAGCA 3600

20 TGAATCCGAC GAACTTTCCT TATGCTCTAT TTCGCTAAAT ACAATTAAAC TTGAAAAGAA 3660

TTGAACTTTT ATTTTATAAT TCGTACTTAT ATATTTTATC CATTAAATTA CAAGTTCATT 3720

25 ATATTATAAT ATATAAATTA TAAGTAATTA ACTTAGAGGT AAAGTTTCTG CTTTACATAC 3780

AGAAGATCAT TGGTTCGATT CCAATATTAC TTAAATAAAT CTATAATTTA ATGGATAAAA 3840

TAAAAACCTT CTAAGTTTAA TATGTAAGTT CAAATCTTAC TAGATTTAAT AATAATGAAT 3900

30 ATGGCGAAAA GGTAACGCG CTAAATTTAG AATTTAGTTT TTATAATAAT AAGAGTTCGA 3960

ATCTCTTTAT TCATATTTAT AATATACTTC TTAACTAGG ATTGAACTAG TATCTTTCGG 4020

35 TTAACAGCCG AATGCTTTAA CCACTAAGCT ATTAAGAATA TTAATATTAT ATTATATAAT 4080

ATATAATAGG GAATATAGTT TAATGGTAAA ATCTTATTCT TGCATAATAA AGATAGTAGT 4140

TCAATTCTAC TTATTTCCAT ATTATAAAAT CTATAAATGT TATAATTTTT AAATAATATA 4200

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TATATAATTA TATTGCGAGT TTGATCCTAG CTCAGAATGA ACGCTAGAAA TATACATTAC 4260
ACATGCAAAT TTATGGATTA TATCATAGTG AATAGGTGAG GATATATAAA TTTTAAATT 4320
5 TAAATAGATT ATAATATATA ATAATCTATA AGCGCATTTA TTTATATAAT TGTACTATAT 4380
TAAAAATTAT TATTGTTTAA AATAAAATTT ATATTTGATT AACTAGTTGG TAAAAATAAA 4440
GCCTACCAAG GTTATGATCA AAAATTGGTT TTAAAGAATG TACAATCACA TTAGGGGATTG 4500
10 AAATAAGGCC CTAAATTTTT TTTAAATCAG CAGTGAGGAA TATTTTACAA TGAGCGTAAG 4560
CTTGATAAAG TAATATTTCT TAAAGGATGA CAGTATATTT TTATATTGTA AACTTTATAT 4620
15 TTTATTTTTA AATATTGATA AAAATAAAAC ATTAGTATTT GCTAATTTCT GTGCCAGCAG 4680
CAGCGGTAAT ACAGAAAATA CCAGCGTTAT TCACTTTATT TGGCGTAAAG CGTTTTAAGG 4740
TTTTATATTA ATTTTATTTT AAAATATTTA ATTTAAATTT GAATAAAAAA TAAATAATAA 4800
20 TATAATAAGA GTATTATAAA AGTATTAAGA ATTTTTTGAG AAGTAGTGAA ATGCAATGAT 4860
ACAAAAAAGA ATACCAAAGG CGAAGGCATA ATACTATATA ATAAGTGACA CTTATAAACG 4920
25 AAAGCTAAGG TAGCAAATAG GATTAGATAC CCTAGTAGTC TTAGCTGTAA ACTATGAATA 4980
TTTTATATTT ATATATTAAT ATAAATATAA TAACTAACGT AATAAATATT CCGCCTGAGT 5040
AGTATATTTC CAAGAACGAA ATTCAAAGGA ATTGACGGGA GCTTATACAA GTGGTGGAAC 5100
30 ATGTGGCTTA ATTCGATGCA ACACGATAAA CCTTACCAA ATTAAACAAT ATTTTTATTA 5160
TTAAGGAATT AATAGTTTAA TAAATATAT AGGTAGTGCA TGGCTGTCGT CAGTTCGTGC 5220
35 TGTGAAGTAT TAATTTAAGT ATTATAACGA ACGTAACCCT TTTATAAAAA AAATTTTTTTA 5280
TAATATATTT ATTAAATATA TAAAAAGAC TACGTCAAGT CATTATGCTC CTTATATTTT 5340
GGGCTGCTCA CGTGTTACAT AAAATATAAC AATATTTTAT TATATGAAAA TATAATATAT 5400
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TAAATATATT TATAGTTCTG ATTATAAATT GAAACTCATT TATATGAAGA TCGAATCACT 5460
 AGTAATCGCT AATAAGAAGT ATAGCGGTGA ATAAGTTCTT AAGCTTTGTA CACACCGCCC 5520
 5 GTCACATCTG GAAAATATTA TATTATATAA AAATTATTGT AAAATAATAA TATATAATTA 5580
 TATAATTTAG ATGAAGTCGT AACCAAGGTAG CCGTACTGGA AGGTGCGGCT GGATAATAAC 5640
 ATAAAATTTT GGTGGAATTA TTTATTTAAA AATAATATTT ATATATAAAA GTAATTATAA 5700
 10 TTATATAATT TTTATAGACA AAAATAGCAT TAATACACAT TAATGTAAAT TTAGTTAAAT 5760
 ATTATTTTAT ATATATAAAG GTTTTTAGTT TAATGGTAAA ACATACTCTT GATAAGGGTA 5820
 15 AGACTTTAGT TCAATTCTAA AATAACCTA 5849

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1711 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TTCAGAAAAA TAGGATTGTA ACCTATATTC TTCTATTCCC AAAATAGATA TGTTACCATT 60
 30 ACACTATATT CTGAATATTT AAAATTTTAT ACTTTTAAGG AAAATCGAAT TCCTATTTTC 120
 TTCTTGAAAA AAAGATGICT TACCTTTAAA CGATAAAAGT AAAAAGTTAA ATTACCTGAG 180
 ACTTGAAGTC AGAACCATTG GATTAAAAGT CGAGTACTCT ACCAATTAAG CTAGTAATTC 240
 35 TTAATATAAC GAATCTGACG AGAATTGAAC TCGTATTCTT TGTATGACA AAATAATATT 300
 TTAACCTAAT TAACTACAA ATTCAAATAA ATATATATAG GGAAAAGGGA TTCGAACCCCT 360
 40 GGTATATATA ATATCTACAT AAATGTAGCA ATTTATAGCT ATAACCACTC AGCCATTTCT 420

GTATATAATA ATAAGTTAAA TCAGATTGAA CTGATGTAGA TATAAAACCC AATGGATTTA 480
CAGTCCATCC CTTTAAACCC CTCAGGCATT AACTTTATTA TACATTAAAG TAGATTTCGAA 540
5 CTACTGATGT TCAATATTTG AAAATGAATT ATGAGTCCAT TGCTTTCGAC CTCTTAGCTA 600
TAAATGTTTA CTTTATTAGA GATAAAGGGA CTCGAACCC TACAACAATT ATTGTTAATG 660
GATTTTCTAA TTGAAATTGA GACTTTTAT AAACATGTAT ATAAATAATA AAGTCGTTTG 720
10 AATATATAAC TAATATATTA CAGAATAAAA ATTATTTTTT CTTTATATAT ATTTAAATTA 780
TTAATTTATT TATAAAATTA ACTCATAAAC AACGAATATA AATTATATTT ATATTATTTA 840
15 AAGTCCATTG TGTATACCAA ATTCACCAT ATCTCTATTA TATACTATAT AAATGATATT 900
CAGATTTGAA CTGAAATAAA ATAATTTGCA ATTATCCACT TTACCTAATT AAGTTATATC 960
ATTATTATAT ATTATAAGAT AAATAAAGAG ATTGAACTC ATATAAAGA AACCACAATT 1020
20 CCTATCTTA ACCTTTAGGA TTATATTTAT CATTATTAAA ACTTATTATA TATTATAAAT 1080
ATTATTATAA ATATATAAAA TATTATTTAA ATATAAATCA TTTAATATTT TTATTTTAAA 1140
25 ATTATATATA CATATAATAA AATTATCATT AAAACTAGAA GATTTAATAA AATTATATTT 1200
ATATAAATTT GATATATAAA TATATATATT ATATCTATAA ATTAAATTTG GTGAAATTAT 1260
ATATTTAATT TTTTATTAA AAAAAATTAT ATCCTTACCC TTTAATTTAA TATTATAATA 1320
30 ATTACCATAA ACCTTATTTA AATATACATA TTTATACCTT ATATAATATC TCAGAGTGGT 1380
GTATAGTTTT AAAAACCCCA TATTAECTAA AAAGACATCT AATCTAGGTT CTAATAGATT 1440
35 TAATAATTTG AGATATAAAT GATTCTCATG GTGACTCTGT ATTTTTTTCA AATAATGTAA 1500
ATATGGTTTA AATGTTATAC CATAATTATA ACAGATATAT CTTACAAATT TTAATTTTAA 1560
ATCGAAATAA GATTGATAGA CATATTTATT AATTTTAAAT TTATAATTAT ATTTACTAGA 1620
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TAAATATAAT AAAAAAGGAA GATTTAATTT TTTTAACATT TTTATTTTAG GAGTTAAAAA 1680

TTTATCATA ATAATTTTAT ATTATAAAAT A 1711

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 516 base pairs

(B) TYPE: nucleic acid

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(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Plasmodium berghei

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(vii) IMMEDIATE SOURCE:

(B) CLONE: CLONE PRB

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTAATAGACA TGGACATAAA GGTGTTATTT CTTATATTAA TGATATTAAT GATATGCCTT 60

ATTTAAATAA CAAAATACAA CCTGATTAT TGTAAAGTGC TATTGGTATA CCTTCTAGAA 120

25

TAAATATAGG TCAAATATTA GAGGGTATAT ATGGATTAAA TAGTTTATAT TTAAATAATA 180

GATATATAAT ATCTAATAAT TTAAATACTA ATTATTATAA TAATTATATT AATAATTTTA 240

30 ATTATTATAA ATATAATTAT AATAATAATT TTGAATTCAA TAAAATATCA TATAATTATA 300

ATAAAATATTT TTTAAAAAAT CCGTTTACGG GCCATTTAAT ACAGAATAGT ATTTGTTTAA 360

ATAATATTTA TTATTATAAA TTAGTACATA TGGTAAAAGA TAAATTAAGA TATAGATTCA 420

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TAGGATTATA TTCTGAATTA ACTCAACAAC CTGTAAAAGG AAATACAAAA CAAGGAGGTC 480

AAAGATTGGG TGAAATGGAA GTATGGGCGC TAGAAG 516

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 base pairs

(B) TYPE: nucleic acid

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(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Plasmodium berghei

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(vii) IMMEDIATE SOURCE:

(B) CLONE: CLONE PWQ

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTTCAAAAAT CAGATTGAC TGATAACACA TGGAACTTCA ATCCATTGCT CTACCATTGA 60

GCTATAATGA CTTAATAATA TTATTATTAT AATAGAATAT AACCAAAAGG TTAAGGTAAT 120

GAACTTTGAT TTCATTAAATA TAGGTTTCGAA TCCTTTAGGA C 161

25 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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GACCTGCATG AAAGATG

17

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(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTATCGCTTT AATAGGCG

18

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCACTACTA TGAAAATC

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGTTTCATTC TGAGCTAG

13

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGGTAATAC AGAAAATGCA AGCG

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGCACGAACT GACGACAGCC ATGCAC

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(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAGGAATA CGTCTAGG

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(2) INFORMATION FOR SEQ ID NO:12:

- 5 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15 GCTAGTATTA TGTCTTCT

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(2) INFORMATION FOR SEQ ID NO:13:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CACCATTAAG TACATCAC

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(2) INFORMATION FOR SEQ ID NO:14:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

5 TGTTAATACA ACTCCAAT

18

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCTAGTATTA TGTCTTCA

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(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGAATGTTAT TGCTAACAC

19

(2) INFORMATION FOR SEQ ID NO:17:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

5 GTAATCAATC TATGATAC

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(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AATGAAGAGC TGTGTATC

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20 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

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GCGATAAGCC GACATCGAGG TGCC

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

5 TATCGTGTG CATCGAATTA AGCC

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(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCTCGACTAC CATTTTAATA TCAATACCTA CCGGTA

36

20 (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

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AGGTGCAATT ATTGCATTGT TTACATTAGT AAGTA

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